

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Rhode, Peter R.
Acevdo, Jorge
Burkhardt, Martin
Jiao, Jin-an
Wong, Hing C.
- (ii) TITLE OF THE INVENTION: SOLUBLE MHC COMPLEXES AND
METHODS OF USE THEREOF
- (iii) NUMBER OF SEQUENCES: 35
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
(B) STREET: 130 Water Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Corless, Peter F
(B) REGISTRATION NUMBER: 33,860
(C) REFERENCE/DOCKET NUMBER: 46561
- (ix) TELECOMMUNICATION INFORMATION:
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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

8

- (i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

43

- (i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

34

- (i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

37

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGCGACTA GTCCACTCCA CAGTGATGGG GC

32

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGGGGGCCA TGGCCGAAGA CGACATTGAG GCCGAC

36

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCGACTAG TCCAGTGTTT CAGAACCGGC TC

32

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGGGGGATA TCTCTCAGGC TGTTACGCT G

31

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGGGTTCG AAAAGTGTAC TTACGGGGGG CTGGAATCTC AGGTTC

46

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGGGGCTCG AGTATCAAAG AAGAACATGT GATCATC

37

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGGCGGGAT CCGTTCTCTG TAGTCTCTGG GAGAGG

36

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATAAGAGGA AGAAGAGTAC ATGCCGATGG AACCCGGGTG AG

42

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

TOP SECRET

43

60
75

48

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

32

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

33

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

33

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

24

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

24

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCCCCACC GGTACGACAA GCCCGTGGTG

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCCCCATCG ATAAGTGTAC TTACGTGGGA GAGGGCTTGG AGCAT

45

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 6...1505
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCACC	ATG	GCT	CTG	CAG	ATC	CCC	AGC	CTC	CTC	CTC	TCA	GCT	GCT	GTG	GTG	50
Met	Ala	Leu	Gln	Ile	Pro	Ser	Leu	Leu	Leu	Ser	Ala	Ala	Val	Val		
1				5						10					15	

GTG	CTG	ATG	GTG	CTG	AGC	AGC	CCA	AGG	ACC	TTA	AGT	ATC	TCT	CAG	GCT	98
Val	Leu	Met	Val	Leu	Ser	Ser	Pro	Arg	Thr	Leu	Ser	Ile	Ser	Gln	Ala	
			20						25					30		

GTT	CAC	GCT	GCT	CAC	GCT	GAA	ATC	AAC	GAA	GCT	GGT	CGT	GCT	AGC	GGA	146
Val	His	Ala	Ala	His	Ala	Glu	Ile	Asn	Glu	Ala	Gly	Arg	Ala	Ser	Gly	
			35					40						45		

GGG Gly	GGC Gly	GGA Gly	AGC Ser	GGC Gly	GGA Gly	GGG Gly	GGA Gly	AAC Asn	TCC Ser	GAA Glu	AGG Arg	CAT His	TTC Phe	GTG Val	GTC Val	194
50																
55																
60																
CAG Gln	TTC Phe	AAG Lys	GGC Gly	GAG Glu	TGC Cys	TAC Tyr	TAC Tyr	ACC Thr	AAC Asn	GGG Gly	ACG Thr	CAG Gln	CGC Arg	ATA Ile	CGG Arg	242
65																
70																
75																
CTC Leu	GTG Val	ACC Thr	AGA Arg	TAC Tyr	ATC Ile	TAC Tyr	AAC Asn	CGG Arg	GAG Glu	GAG Glu	TAC Tyr	GTG Val	CGC Arg	TAC Tyr	GAC Asp	290
80																
85																
90																
AGC Ser	GAC Asp	GTG Val	GGC Gly	GAG Glu	TAC Tyr	CGC Arg	GCG Ala	GTG Val	ACC Thr	GAG Glu	CTG Leu	GGG Gly	CGG Arg	CCA Pro	GAC Asp	338
100																
105																
110																
GCC Ala	GAG Glu	TAC Tyr	TGG Trp	AAC Asn	AGC Ser	CAG Gln	CCG Pro	GAG Glu	ATC Ile	CTG Leu	GAG Glu	CGA Arg	ACG Thr	CGG Arg	GCC Ala	386
115																
120																
125																
GAG Glu	GTG Val	GAC Asp	ACG Thr	GCG Ala	TGC Cys	AGA Arg	CAC His	AAC Asn	TAC Tyr	GAG Glu	GGG Gly	CCG Pro	GAG Glu	ACC Thr	AGC Ser	434
130																
135																
140																
ACC Thr	TCC Ser	CTG Leu	CGG Arg	CGG Arg	CTT Leu	GAA Glu	CAG Gln	CCC Pro	AAT Asn	GTC Val	GCC Ala	ATC Ile	TCC Ser	CTG Leu	TCC Ser	482
145																
150																
155																
AGG Arg	ACA Thr	GAG Glu	GCC Ala	CTC Leu	AAC Asn	CAC His	CAC His	AAC Asn	ACT Thr	CTG Leu	GTC Val	TGT Cys	TCG Ser	GTG Val	ACA Thr	530
160																
165																
170																
GAT Asp	TTC Phe	TAC Tyr	CCA Pro	GCC Ala	AAG Lys	ATC Ile	AAA Lys	GTG Val	CGC Arg	TGG Trp	TTC Phe	AGG Arg	AAT Asn	GGC Gly	CAG Gln	578
180																
185																
190																
GAG Glu	GAG Glu	ACA Thr	GTG Val	GGG Gly	GTC Val	TCA Ser	TCC Ser	ACA Thr	CAG Gln	CTT Leu	ATT Ile	AGG Arg	AAT Asn	GGG Gly	GAC Asp	626
195																
200																
205																
TGG Trp	ACC Thr	TTC Phe	CAG Gln	GTC Val	CTG Leu	GTC Val	ATG Met	CTG Leu	GAG Glu	ATG Met	ACC Thr	CCT Pro	CAT His	CAG Gln	GGA Gly	674
210																
215																
220																
GAG Glu	GTC Val	TAC Tyr	ACC Thr	TGC Cys	CAT His	GTG Val	GAG Glu	CAT His	CCC Pro	AGC Ser	CTG Leu	AAG Lys	AGC Ser	CCC Pro	ATC Ile	722
225																
230																
235																
ACT Thr	GTG Val	GAG Glu	TGG Trp	ACT Thr	AGT Ser	GGT Gly	GGC Gly	GGT Gly	GGC Gly	AGC Ser	GGC Gly	GGT Gly	GGT Gly	GGT Gly	TCC Ser	770
240																
245																
250																
255																
GGT Gly	GGC Gly	GGC Gly	GGT Gly	TCT Gly	GGC Gly	GGT Gly	GGC Gly	GGT Gly	TCC Gly	TCG Gly	AGT Gly	GAA Gly	GAC Gly	GAC Gly	ATT Gly	818

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Glu	Asp	Asp	Ile			
260					265					270							
GAG	GCC	GAC	CAC	GTA	GGC	TTC	TAT	GGT	ACA	ACT	GTT	TAT	CAG	TCT	CCT	866	
Glu	Ala	Asp	His	Val	Gly	Phe	Tyr	Gly	Thr	Thr	Val	Tyr	Gln	Ser	Pro		
275					280					285							
GGA	GAC	ATT	GGC	CAG	TAC	ACA	CAT	GAA	TTT	GAT	GGT	GAT	GAG	TTG	TTC	914	
Gly	Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu	Phe	Asp	Gly	Asp	Glu	Leu	Phe		
290					295					300							
TAT	GTG	GAC	TTG	GAT	AAG	AAG	AAA	ACT	GTC	TGG	AGG	CTT	CCT	GAG	TTT	962	
Tyr	Val	Asp	Leu	Asp	Lys	Lys	Lys	Thr	Val	Trp	Arg	Leu	Pro	Glu	Phe		
305					310					315							
GGC	CAA	TTG	ATA	CTC	TTT	GAG	CCC	CAA	GGT	GGA	CTG	CAA	AAC	ATA	GCT	1010	
Gly	Gln	Leu	Ile	Leu	Phe	Glu	Pro	Gln	Gly	Gly	Leu	Gln	Asn	Ile	Ala		
320					325					330					335		
GCA	GAA	AAA	CAC	AAC	TTG	GGA	ATC	TTG	ACT	AAG	AGG	TCA	AAT	TTC	ACC	1058	
Ala	Glu	Lys	His	Asn	Leu	Gly	Ile	Leu	Thr	Lys	Arg	Ser	Asn	Phe	Thr		
340					345					350							
CCA	GCT	ACC	AAT	GAG	GCT	CCT	CAA	GCG	ACT	GTG	TTC	CCC	AAG	TCC	CCT	1106	
Pro	Ala	Thr	Asn	Glu	Ala	Pro	Gln	Ala	Thr	Val	Phe	Pro	Lys	Ser	Pro		
355					360					365							
GTG	CTG	CTG	GGT	CAG	CCC	AAC	ACC	CTT	ATC	TGC	TTT	GTG	GAC	AAC	ATC	1154	
Val	Leu	Leu	Gly	Gln	Pro	Asn	Thr	Leu	Ile	Cys	Phe	Val	Asp	Asn	Ile		
370					375					380							
TTC	CCA	CCT	GTG	ATC	AAC	ATC	ACA	TGG	CTC	AGA	AAT	AGC	AAG	TCA	GTC	1202	
Phe	Pro	Pro	Val	Ile	Asn	Ile	Thr	Trp	Leu	Arg	Asn	Ser	Lys	Ser	Val		
385					390					395							
ACA	GAC	GGC	GTT	TAT	GAG	ACC	AGC	TTC	CTC	GTC	AAC	CGT	GAC	CAT	TCC	1250	
Thr	Asp	Gly	Val	Tyr	Glu	Thr	Ser	Phe	Leu	Val	Asn	Arg	Asp	His	Ser		
400					405					410					415		
TTC	CAC	AAG	CTG	TCT	TAT	CTC	ACC	TTC	ATC	CCT	TCT	GAT	GAT	GAC	ATT	1298	
Phe	His	Lys	Leu	Ser	Tyr	Leu	Thr	Phe	Ile	Pro	Ser	Asp	Asp	Asp	Ile		
420					425					430							
TAT	GAC	TGC	AAG	GTG	GAG	CAC	TGG	GGC	CTG	GAG	GAG	CCG	GTT	CTG	AAA	1346	
Tyr	Asp	Cys	Lys	Val	Glu	His	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu	Lys		
435					440					445							
CAC	TGG	GAA	CCT	GAG	ATT	CCA	GCC	CCC	ATG	TCA	GAG	CTG	ACA	GAA	ACT	1394	
His	Trp	Glu	Pro	Glu	Ile	Pro	Ala	Pro	Met	Ser	Glu	Leu	Thr	Glu	Thr		
450					455					460							
GTG	GTG	TGT	GCC	CTG	GGG	TTG	TCT	GTG	GGC	CTT	GTG	GGC	ATC	GTG	GTG	1442	
Val	Val	Cys	Ala	Leu	Gly	Leu	Ser	Val	Gly	Leu	Val	Gly	Ile	Val	Val		
465					470					475							

245 250 255
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Asp Asp Ile Glu
 260 265 270
 Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly
 275 280 285
 Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr
 290 295 300
 Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly
 305 310 315 320
 Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala
 325 330 335
 Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro
 340 345 350
 Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val
 355 360 365
 Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe
 370 375 380
 Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr
 385 390 395 400
 Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe
 405 410 415
 His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr
 420 425 430
 Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His
 435 440 445
 Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val
 450 455 460
 Val Cys Ala Leu Gly Leu Ser Val Gly Leu Val Gly Ile Val Val Gly
 465 470 475 480
 Thr Ile Phe Ile Ile Gln Gly Leu Arg Ser Gly Gly Thr Ser Arg His
 485 490 495
 Pro Gly Pro Leu
 500

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

Ala Pro Tyr Ser Thr Leu Leu Pro Pro Glu Leu Ser Glu Thr Pro
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Tyr Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro
1 5 10 15
Arg Thr Pro Pro
20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Glu Glu Glu Glu Tyr Met Pro Met Glu Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TSGGGGSGGG GSGGGGSGGG GSSS

24

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg
1 5 10 15
Thr Pro Pro

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ser Ser Ala Asp Leu Val Pro Arg Gly Ser Thr Thr Ala Pro Ser Ala
1 5 10 15
Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu
20 25 30
Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln
35 40 45

(2) INFORMATION FOR SEQ ID NO:34:

- (A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser	Ser	Ala	Asp	Leu	Val	Pro	Arg	Gly	Ser	Thr	Thr	Ala	Pro	Arg	Ala
1				5					10					15	
Gln	Leu	Lys	Lys	Lys	Leu	Gln	Ala	Leu	Lys	Lys	Lys	Asn	Ala	Gln	Leu
		20						25					30		
Lys	Trp	Lys	Leu	Gln	Ala	Leu	Lys	Lys	Leu	Ala	Gln				
		35					40								

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ASSGGGSGGG

10